



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 146887

TO: Emily M Le
Location: 3c35/3c18
Art Unit: 1648
Thursday, March 10, 2005

Case Serial Number: 09/939537

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 06:29:55 ; Search time 3106 Seconds
(without alignments)
9411.899 Million cell updates/sec

Title: US-09-939-537-32

Perfect score: 768
Sequence: 1 GCTAGCAGACCCAAATCTT.....GGCTCTGCACGCGATCC 768

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	736.6	95.9	881	5	BQ711291	BQ711291 AGENCOURT
2	691.2	90.0	871	4	BG753979	BG753979 602709506
3	691.2	90.0	983	5	BQ708975	BQ708975 AGENCOURT
4	690.2	89.9	897	5	BQ709144	BQ709144 AGENCOURT
5	690.2	89.9	941	5	BQ712021	BQ712021 AGENCOURT
6	689.6	89.8	843	4	BM007897	BM007897 603617582
7	689.6	89.8	925	5	BQ709152	BQ709152 AGENCOURT
8	689.6	89.8	1022	3	CR611254	CR611254 full-leng
9	689.6	89.8	1048	3	CR595172	CR595172 full-leng
10	689.6	89.8	1090	3	CR612308	CR612308 full-leng
11	689.6	89.8	1091	3	CR604961	CR604961 full-leng
12	689.6	89.8	1093	3	CR616804	CR616804 full-leng
13	689.6	89.8	1098	3	CR626477	CR626477 full-leng
14	689.6	89.8	1100	3	CR612813	CR612813 full-leng
15	689.6	89.8	1102	3	CR601777	CR601777 full-leng
16	689.6	89.8	1102	3	CR625051	CR625051 full-leng
17	689.6	89.8	1103	3	CR595194	CR595194 full-leng
18	689.6	89.8	1104	3	CR591904	CR591904 full-leng
19	689.6	89.8	1106	3	CR613460	CR613460 full-leng
20	689.6	89.8	1106	3	CR620071	CR620071 full-leng
21	689.6	89.8	1107	3	CR598548	CR598548 full-leng
22	689.6	89.8	1109	3	CR614200	CR614200 full-leng
23	689.6	89.8	1109	3	CR619687	CR619687 full-leng
24	689.6	89.8	1111	3	CR606782	CR606782 full-leng

25	689.6	89.8	1114	3	CR593349	CR593349 full-leng
26	689.6	89.8	1114	3	CR618075	CR618075 full-leng
27	689.6	89.8	1118	3	CR613511	CR613511 full-leng
28	689.6	89.8	1120	3	CR619868	CR619868 full-leng
29	689.6	89.8	1124	3	CR611468	CR611468 full-leng
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31	689.6	89.8	1142	3	CR598316	CR598316 full-leng
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33	689.6	89.8	1287	3	CR611016	CR611016 full-leng
34	689.6	89.8	1289	3	CR594000	CR594000 full-leng
35	688.6	89.7	851	5	BX346946	BX346946 BX346946
36	688.6	89.7	973	5	BQ706204	BQ706204 AGENCOURT
37	688	89.6	919	5	BQ709339	BQ709339 AGENCOURT
38	686.4	89.4	947	5	BQ709771	BQ709771 AGENCOURT
39	685.8	89.3	856	5	BQ709859	BQ709859 AGENCOURT
40	685.4	89.2	914	5	BQ712363	BQ712363 AGENCOURT
41	684.2	89.1	1013	5	BX360518	BX360518 BX360518
42	683.8	89.0	757	4	BG674795	BG674795 602620925
43	683.2	89.0	902	5	BUI46962	BUI46962 AGENCOURT
44	679.2	88.4	892	4	BG397723	BG397723 602438784
45	679.2	88.4	897	4	BM008412	BM008412 603617406

ALIGNMENTS

RESULT 1
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LOCUS BQ711291 881 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096
5', mRNA sequence.
ACCESSION BQ711291
VERSION BQ711291
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 881)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM2468 row: c column: 01
High quality sequence stop: 721.
Location/Qualifiers
source
1. .881
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6279096"
/lab_host="NIH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 95.9%; Score 736.6; DB 5; Length 881;
Best Local Similarity 98.2%; Pred. No. 8.4e-169;

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

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Query Match      89.9%; Score 690.2; DB 5; Length 897;
Best Local Similarity 99.6%; Pred. No. 1.7e-157;
Matches 692; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTGTGACAAAACCTCACATGCCACCGTGCAGCAGCACTGAATC 63
Db 31 AGTTGAGCCCAATCTGTGACAAAACCTCACATGCCACCGTGCAGCAGCACTGAATC 90
QY 64 CTTGGGGGAGCCGTCAGTCTTCTCTTCCCCCAAAACCCAGGACACCCCTCATGATCTC 123
Db 91 CTTGGGGGAGCCGTCAGTCTTCTCTTCCCCCAAAACCCAGGACACCCCTCATGATCTC 150
QY 124 CCGGACCCCTGAGGTGCATGCGTGGTGGACGTGAGCCACGAGACCCCTGAGGTCAA 183
Db 151 CCGGACCCCTGAGGTGCATGCGTGGTGGACGTGAGCCACGAGACCCCTGAGGTCAA 210
QY 184 GTTCAACTGCTACGTGAGCGGCTGGAGTGCATATGCCAAGACAAAGCCGCGGAGGA 243
Db 211 GTTCAACTGCTACGTGAGCGGCTGGAGTGCATATGCCAAGACAAAGCCGCGGAGGA 270
QY 244 GCAGTACAAACAGCAGTACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 303
Db 271 GCAGTACAAACAGCAGTACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 330
QY 304 GAATGGCAAGGAGTACAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 363
Db 331 GAATGGCAAGGAGTACAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 390
QY 364 AACCATCTCCAAAGCCAAAGGCGCCCGGAGAACCAAGTGTACACCTGCCCCCATC 423
Db 391 AACCATCTCCAAAGCCAAAGGCGCCCGGAGAACCAAGTGTACACCTGCCCCCATC 450
QY 424 CCGGATGAGCTGACCAAGAACCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 483
Db 451 CCGGATGAGCTGACCAAGAACCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 510
QY 484 CAGCGACATCGCGTGGAGTGGAGAGCAATGGGCAACCGGAGAACCAACTACAGACCAAC 543
Db 511 CAGCGACATCGCGTGGAGTGGAGAGCAATGGGCAACCGGAGAACCAACTACAGACCAAC 570
QY 544 GCCTCCCGTGTGAGTCCGACCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 603
Db 571 GCCTCCCGTGTGAGTCCGACCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 630
QY 604 GAGCAGTGGCAGCAGGGGAAACGTTCTTCTCATGCTCCGATGATGAGGTCTTCACAA 663
Db 631 GAGCAGTGGCAGCAGGGGAAACGTTCTTCTCATGCTCCGATGATGAGGTCTTCACAA 690
QY 664 CCACTACGCGAGAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 698
Db 691 CCACTACGCGAGAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 725

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RESULT 5

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BQ712021
LOCUS      BQ712021
DEFINITION AGENCOURT_8418162 NIH_MGC_113 Homo sapiens linear EST 16-JUL-2002
5', mRNA sequence.
ACCESSION BQ712021
VERSION   BQ712021.1
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 941)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.

```

TITLE
JOURNAL
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.G.E. Consortium information can be
http://image.llnl.gov
Plate: LLCM2474 row: c column: 04
High quality sequence stop: 638.

FEATURES
source

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1..941
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6281403"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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ORIGIN

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Query Match      89.9%; Score 690.2; DB 5; Length 941;
Best Local Similarity 99.4%; Pred. No. 1.8e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAAACCTCACATGCCACCGTGCAGCAGCACTGAATC 63
Db 31 AGTTGAGCCCAATCTTGTGACAAAACCTCACATGCCACCGTGCAGCAGCACTGAATC 90
QY 64 CTTGGGGGAGCCGTCAGTCTTCTTCTTCCCAAAACCCAGGACACCCCTCATGATCTC 123
Db 91 CTTGGGGGAGCCGTCAGTCTTCTTCTTCCCAAAACCCAGGACACCCCTCATGATCTC 150
QY 124 CCGGACCCCTGAGTGCATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 183
Db 151 CCGGACCCCTGAGTGCATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 210
QY 184 GTTCAACTGCTACGTGAGCGGCTGGAGTGCATATGCCAAGACAAAGCCGCGGAGGA 243
Db 211 GTTCAACTGCTACGTGAGCGGCTGGAGTGCATATGCCAAGACAAAGCCGCGGAGGA 270
QY 244 GCAGTACAAACAGCAGTACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 303
Db 271 GCAGTACAAACAGCAGTACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 330
QY 304 GAATGGCAAGGAGTACAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 363
Db 331 GAATGGCAAGGAGTACAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 390
QY 364 AACCATCTCCAAAGCCAAAGGCGCCCGGAGAACCAAGTGTACACCTGCCCCCATC 423
Db 391 AACCATCTCCAAAGCCAAAGGCGCCCGGAGAACCAAGTGTACACCTGCCCCCATC 450
QY 424 CCGGATGAGCTGACCAAGAACCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 483
Db 451 CCGGATGAGCTGACCAAGAACCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 510
QY 484 CAGCGACATCGCGTGGAGTGGAGAGCAATGGGCAACCGGAGAACCAACTACAGACCAAC 543
Db 511 CAGCGACATCGCGTGGAGTGGAGAGCAATGGGCAACCGGAGAACCAACTACAGACCAAC 570
QY 544 GCCTCCCGTGTGAGTCCGACCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 603

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Db      571  GCCTCCGCTGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGACAA 630
Qy      604  GAGCAGGTGGCAGCAGGGAACGTCTTCTCATCTCCGTGATGCATGAGGCTCTGCACAA 663
Db      631  GAGCAGGTGGCAGCAGGGAACGTCTTCTCATCTCCGTGATGCATGAGGCTCTGCACAA 690
Qy      664  CCACTACAGCAGAGAGGCTCTCTCTGCTCTCCGG 699
Db      691  CCACTACAGCAGAGAGGCTCTCTCTGCTCTCCGG 726

RESULT 6
BM007897 843 bp mRNA linear EST 30-OCT-2001
LOCUS 603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
DEFINITION mRNA sequence.
ACCESSION BM007897
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 843)
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: d column: 22
High quality sequence stop: 833.
Location/Qualifiers
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/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 89.8%; Score 689.6; DB 4; Length 843;
Best Local Similarity 99.4%; Pred. No. 2.4e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 AGCAGAGCCCAATCTTGTGACAAACTCACACATGCCCGCCAGCAGCCTGAACT 63
Db 89 AGTTGAGCCCAATCTTGTGACAAACTCACACATGCCCGCCAGCAGCCTGAACT 148
Qy 64 CTGGGGGACCGTCACTCTCTCTCCCAAAACCCAGGACACCTCATGATCTC 123
Db 149 CTGGGGGACCGTCACTCTCTCTCTCCCAAAACCCAGGACACCTCATGATCTC 208
Qy 124 CCGGACCCCTGAGGTCAACATGGCTGGTGGAGCGTGGAGCCAGAGCCCTGAGGTCAA 183
Db 209 CCGGACCCCTGAGGTCAACATGGCTGGTGGAGCGTGGAGCCAGAGCCCTGAGGTCAA 268
Qy 184 GTTCAACTGGTACGTGGAGCGGCGTGGAGGTGCATTAATGCCAAGAACCCCGGGAGGA 243

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Db      269  GTTCAACTGGTACGTGGAGCGGCTGCATTAATGCCAAGAACCCCGGGAGGA 328
Qy      244  GCAGTACAACACGATACCGGGTGGTCCAGCGTCTCTACCGTCTCTGCACGAGGCTGGCT 303
Db      329  GCAGTACAACACGATACCGGTGGTCCAGCGTCTCTACCGTCTCTGCACGAGGCTGGCT 388
Qy      304  GAATGGCAAGGATACAAGTGCAGGTCTTCAAAAGCCCTCCAGCCCCCATCGAGAA 363
Db      389  GAATGGCAAGGATACAAGTGCAGGTCTTCAAAAGCCCTCCAGCCCCCATCGAGAA 448
Qy      364  RACCATCTCCAAAGCCAGCCGAGCAACACAGGTGTACACCTGCCCCCATC 423
Db      449  RACCATCTCCAAAGCCAGCCGAGCAACACAGGTGTACACCTGCCCCCATC 508
Qy      424  CCGGATGAGCTGACCAAGAACAGGTGAGCTGCTGCTGCTCAAAAGGCTTTCTATCC 483
Db      509  CCGGATGAGCTGACCAAGAACAGGTGAGCTGCTGCTGCTCAAAAGGCTTTCTATCC 568
Qy      484  CAGCAGATCGCCGTGGAGTGGAGAGCAATGGGAGCGCGGAGAACAACTACAGACCAC 543
Db      569  CAGCAGATCGCCGTGGAGTGGAGAGCAATGGGAGCGCGGAGAACAACTACAGACCAC 628
Qy      544  GCCTCCCGTGGTGGACTCCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAA 603
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Qy      604  GAGCAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 663
Db      689  GAGCAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 748
Qy      664  CCATTACAGCAGAGAGGCTCTCCCTGTCTCCGG 699
Db      749  CCATTACAGCAGAGAGGCTCTCCCTGTCTCCGG 784

RESULT 7
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LOCUS AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245
DEFINITION 5', mRNA sequence.
ACCESSION BM007897
VERSION 1
KEYWORDS EST.
SOURCE BM007897:1 GI:21848051
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: m column: 22
High quality sequence stop: 739.
Location/Qualifiers
1. .925
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/clone_lib="NIH MGC 113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned

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QY 664 CCCTACACGACGAGAGAGCTCTCCCTGCTCTCCGGG 699
Db 964 CCCTACACACAGAGAGGCTCTCCCTGCTCTCCGGG 999

RESULT 9
LOCUS CR595172 1048 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1040YA16 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR595172
VERSION CR595172.1 GI:50475979
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1048)
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1048)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
1..1048
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1040YA16"
/tissue_type="Placenta Cot 25-normalized"
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ORIGIN
Query Match 89.8%; Score 689.6; DB 3; Length 1048;
Best Local Similarity 99.4%; Pred. No. 2.5e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGACAAACTCACATGTCGCCACCGTCCCGACACCTGAACT 63
Db 317 AGTTGAGCCCAATCTTGACAAACTCACATGTCGCCACCGTCCCGACACCTGAACT 376
QY 64 CTGCGGGGACCGTCAGTCTTCTTCTCCCAAAACCCCAAGGACACCTCATGATCTC 123
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QY 124 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 183
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Db 497 GTTCAACTGGTACGTGGAGCGGTGGAGTGGATATGTCACAGACAAAGCCCGGGAGA 556
QY 244 GCAGTACAAACAGCAGTACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 303
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Db 677 AACCATCTCCAAAGCAAAAGGCGAGCCCGGAGAACACAGAGTGTACACCTGCCCCATC 736
QY 424 CCGGATGAGTGAACCAAGAACAGGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 483
Db 737 CCGGATGAGTGAACCAAGAACAGGTGAGCTGAGCTGAGCTGCTGCTGCTGCTGCTGCT 796
QY 484 CAGCAGACATCCCGTGGAGTGGAGAGCAATGGGAGCCCGGAGAACACTACAAGACCA 543
Db 797 CAGCAGACATCCCGTGGAGTGGAGAGCAATGGGAGCCCGGAGAACACTACAAGACCA 856
QY 544 GCCTCCCGTGGTGGACTCCGACGGCTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCT 603
Db 857 GCCTCCCGTGGTGGACTCCGACGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 916
QY 604 GAGCAGGTGGCAGCAGGGAAGCTTCTTCTATGCTCCGTCGTCATGAGGCTCTGACAA 663
Db 917 GAGCAGGTGGCAGCAGGGAAGCTTCTTCTATGCTCCGTCGTCATGAGGCTCTGACAA 976
QY 664 CCCTACACGACGAGAGCGCTCTCCCTGCTCTCCGGG 699
Db 977 CCCTACACACAGAGCGCTCTCCCTGCTCTCCGGG 1012

RESULT 10
LOCUS CR612308 1090 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1071YG21 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR612308
VERSION CR612308.1 GI:50493115
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1090)
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1090)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1071YG21"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 89.8%; Score 689.6; DB 3; Length 1090;
Best Local Similarity 99.4%; Pred. No. 2.5e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTCGACAAACTCACATGTCGCCACCGTCCCGACACCTGAACT 63
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Db 304 AGTTGAGCCCAATCTTTGTGACAAACTCACATGCCACCGTCCAGCACCTGAAT 363
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Db 364 CTGTGGGGGACCGTCACTCTTCTTCCGCCCAAAACCCAGGACACCTCATGATCTC 423
Qy 124 CCGGACCCCTGAGGTACATGCTGCTGTGGTGGAGCTGAGCCAGGAGACCTGAGGTCAA 183
Db 424 CCGGACCCCTGAGGTACATGCTGCTGTGGTGGAGCTGAGCCAGGAGACCTGAGGTCAA 483
Qy 184 GTTCAAATGCTGAGTGGAGCGGTGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 243
Db 484 GTTCAAATGCTGAGTGGAGCGGTGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 543
Qy 244 GCAGTACACAGCACGTACCGGTGTGCTGAGCTGCTCAGCTGCTGACAGGACGTGGCT 303
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Qy 304 GAATGCAAGGAGTACAGTGTCAAGTCTTCCAAAGAGCCCTCCAGCCCCCATCGAGAA 363
Db 604 GAATGCAAGGAGTACAGTGTCAAGTCTTCCAAAGAGCCCTCCAGCCCCCATCGAGAA 663
Qy 364 AACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAACCAAGGTGTACACCTGCCCCCATC 423
Db 664 AACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAACCAAGGTGTACACCTGCCCCCATC 723
Qy 424 CCGGATGAGTGCACCAAGAACCAAGTGCAGCTGAGCTGCTGCTGCTCAAGGCTTCTATCC 483
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Qy 664 CCACTACACGACAGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 699
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RESULT 11

CR604961

LOCUS

DEFINITION CR604961 1091 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0D1009YJ10 of Placenta Cot 25-normalized

ACCESSION

CR604961

VERSION

CR604961.1 GI:50485768

KEYWORDS

HTC; CDSLT cDNA.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1091)

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Feng Liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Paradise Avenue

2 (bases 1 to 1091)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)- Web : www.genoscope.cns.fr)

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source

1..1091
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Query Match 89.8%; Score 689.6; DB 3; Length 1091;

Best Local Similarity 99.4%; Pred. No. 2.5e-157;

Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 AGCAGAGCCCAAACTCTTGTGACAAACTCACACATGCCACCGTCCAGCACCTGAAT 63

Db 304 AGTTGAGCCCAAACTCTTGTGACAAACTCACACATGCCACCGTCCAGCACCTGAAT 363

Qy 64 CTGTGGGGGACCGTCACTCTTCTTCCGCCCAAAACCCAGGACACCTCATGATCTC 123

Db 364 CTGTGGGGGACCGTCACTCTTCTTCCGCCCAAAACCCAGGACACCTCATGATCTC 423

Qy 124 CCGGACCCCTGAGGTACATGCTGCTGTGGTGGAGCTGAGCCAGGAGACCTGAGGTCAA 183

Db 424 CCGGACCCCTGAGGTACATGCTGCTGTGGTGGAGCTGAGCCAGGAGACCTGAGGTCAA 483

Qy 184 GTTCAAATGCTGAGTGGAGCGGTGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 243

Db 484 GTTCAAATGCTGAGTGGAGCGGTGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 543

Qy 244 GCAGTACACAGCACGTACCGGTGTGCTGAGCTGCTCAGCTGCTTCTTCTTCTTCTTCTTCT 303

Db 544 GCAGTACACAGCACGTACCGGTGTGCTGAGCTGCTCAGCTGCTTCTTCTTCTTCTTCTTCT 603

Qy 304 GAATGCAAGGAGTACAGTGTCAAGTCTTCCAAAGAGCCCTCCAGCCCCCATCGAGAA 363

Db 604 GAATGCAAGGAGTACAGTGTCAAGTCTTCCAAAGAGCCCTCCAGCCCCCATCGAGAA 663

Qy 364 AACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAACCAAGGTGTACACCTGCCCCCATC 423

Db 664 AACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAACCAAGGTGTACACCTGCCCCCATC 723

Qy 424 CCGGATGAGTGCACCAAGAACCAAGTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483

Db 724 CCGGATGAGTGCACCAAGAACCAAGTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783

Qy 484 CAGCGACATCGCGTGGAGTGGAGAGCAATGGGCGAGCCGAGAGAACCACTACAGACCAAC 543

Db 784 CAGCGACATCGCGTGGAGTGGAGAGCAATGGGCGAGCCGAGAGAACCACTACAGACCAAC 843

Qy 544 GCCTCCCGTGTGGACTCCGAGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 603

Db 844 GCCTCCCGTGTGGACTCCGAGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 903

Qy 604 GAGCAGTGGCGAGCAGGGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 663

Db 904 GAGCAGTGGCGAGCAGGGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 963

Qy 664 CCACTACACGACAGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 699

Db 964 CCACTACACGACAGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 999

RESULT 12

CR616804

LOCUS

DEFINITION CR616804 1093 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0D1048YC07 of Placenta Cot 25-normalized
of Homo sapiens (human).


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Db 484 GTTCACTGTTAGCTGACGGCGTGGAGGTGCATATGCCAAGACAAAGCCGCGGAGGA 543
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Qy 304 GAATGCAAGGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTCCCGACCCCTCATCGAGAA 363
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Db 664 AACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGTGTACACCTGACCCCTGCCCCATC 723
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Qy 664 CCATACACAGCAAGAGAGCTCTCCCTGTCTCCGGG 699
Db 964 CCATACACAGCAAGAGAGCTCTCCCTGTCTCCGGG 999

RESULT 14
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DEFINITION of Homo sapiens (human).
ACCESSION CR612813
VERSION 1
KEYWORDS HTG; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1100)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen.
FEATURES
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Best Local Similarity 99.4%; Pred. No. 2.5e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 300 AGTTGAGCCCAAAATCTTTGTGACAAAATCTACATGSCCCACCGTCCCGACGACCTGAACT 359
Qy 64 CTTGGGGGGGACCGTCAAGTCTTCTTCTCCCAAAAACCAAGGACACCTCATGATCTC 123
Db 360 CTTGGGGGGGACCGTCAAGTCTTCTTCTCCCAAAAACCAAGGACACCTCATGATCTC 419
Qy 124 CCGGACCCCTGAGGTGCATGCTGCTGAGCTGAGCCAGCAAGACCCCTCATGATCTC 183
Db 420 CCGGACCCCTGAGGTGCATGCTGCTGAGCTGAGCCAGCAAGACCCCTCATGATCTC 479
Qy 184 GTTCAACTGCTACGTGGAGCGGCTGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGA 243
Db 480 GTTCAACTGCTACGTGGAGCGGCTGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGA 539
Qy 244 GCAGTACACAGCAGCTACCGGGTGGTCAGCGTCTCTCAACCGTCTCTGACACGAGCTGGCT 303
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Db 840 GCCTCCCGTGTGGACTCCGACGGCTCTCTTCTCTCTTACAGCAAGTCAACGTTGGACAA 899
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RESULT 15
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DEFINITION (human).
ACCESSION CR6101777
VERSION 1
KEYWORDS HTG; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 1102)
TITLE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
```

Paraday Avenue
2 (bases 1 to 1102)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Best Local Similarity 99.4%; Pred. No. 2.5e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 300 AGTTGAGCCCAATCTTGTGACAAACTCACACATGCCCGCCAGGACACCTGAACT 359
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 184 GTTCAACTGGTACGTGGACGGCGGTGAGGTGATTAATGCAAGAACCCCGGGAGGA 243
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 540 GCAGTACAAACAGCAGTACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 599
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QY 304 GAATGGCAGGAGTACAGTGAAGTCTTCAACAAAGCCCTCCAGAGCCCATCGAGAA 363
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QY 364 AACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCCCCCATC 423
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 660 AACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCCCCCATC 719
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QY 424 CCGGATGAGCTGACAGAAACAGGTGAGCTGACCTGCTGGTCAAAGGCTTCTATCC 483
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QY 484 CAGCCACATCGCGTGGAGTGGAGGCAATGGCGAGCGGAGAACACTACAAGCCAC 543
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QY 840 GCCTCCCGTGTGGACTCCGAGGGTCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAA 899
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 604 GAGCAGGTGGCAGAGGGGAAAGTCTTCTCTATGCTCCCGTATGATGAGGCTCTGCACAA 663
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QY 900 GAGCAGGTGGCAGAGGGGAAAGTCTTCTCTATGCTCCGATGATGAGGCTCTGCACAA 959
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QY 664 CCACTACAGCAGAGAGCCCTCTCCCTCTCTCCGGG 699
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